

SEQUENCE LISTING



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<120> NEW SYSTEMS FOR THE REGULATION OF GENE EXPRESSION

<130> 564-9005

<140> 09/147,693

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<150> PCT/EP97/04560

<151> 1997-08-21

<150> DE/196 33 698.8

<151> 1996-08-21

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<170> PatentIn Ver. 2.0

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<212> DNA

<213> Lambda-OR-Operator (wild type)

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ctctggcggt gataatggtt gc 82

<210> 2

<211> 82

<212> DNA

<213> Lambda-OR-Operator (mutant)

<400> 2

acgttaaadc tatcaccgca agggataaat atctaacc gcgcgtgttg actatcttac 60

ctctggcggt gataatggtt gc 82

<210> 3

<211> 85

<212> DNA

<213> Lambda-OL-Operator (wild type)

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acatacagat aaccatctgc ggtgataaat tatctctggc ggtgttgaca taaataccac 60

tggcggtgat actgagcaca tcagc 85

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<222> Complement ((106)..(816))

<220>
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aggccactga ctagcgataa ctttccccac aacggaacaa ctctcattgc atgggatcat 180
tgggtactgt ggggttagtg gttgtaaaaa cacctgaccg ctatccctga tcagtttctt 240
gaaggtaaac tcatcacccc caagtctggc tatgcagaaa tcacctggct caacagcctg 300
ctcaggggtca acgagaatta acattccgtc aggaaagctt ggcttggagc ctggttggtgc 360
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gcttacctat ctctccgat cacctttggt aaagggttcta agcttaggtg agaacatccc 480
tgctgaaca tgagaaaaaa caggggtactc atactcactt ctaagtgcgc gctgcatact 540
aacgcgttca tacatctcgt agatttctct ggcgattgaa gggctaaatt cttcaacgct 600
aactttgaga atttttgtaa gcaatgcggc gttataagca tttaatgcat tgatgccatt 660
aaataaagca ccaacgcctg actgccccat ccccatcttg tctgcgacag attcctggga 720
taagccaagt tcatttttct ttttttcata aattgcttta aggcgacgtg cgtcctcaag 780
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gtaacaaagt ttggattgct actgaccgct ctgctgctcg tcgctgcgtt gaggcttgcg 1140
ttt atg gta cgc tgg act ttg tgg gat acc ctc gct ttc ctg ctc ctg 1188
Met Val Arg Trp Thr Leu Trp Asp Thr Leu Ala Phe Leu Leu Leu
1 5 10 15
ttg agt tta ttg ctg ccg tca ttg ctt att atg ttc atc ccg tca aca 1236
Leu Ser Leu Leu Leu Pro Ser Leu Leu Ile Met Phe Ile Pro Ser Thr
20 25 30
ttc aaa cgg cct gtc tca tca tgg aag gcg ctg aat tta cgg aaa aca 1284

a!
cont

Phe Lys Arg Pro Val Ser Ser Trp Lys Ala Leu Asn Leu Arg Lys Thr
 35 40 45
 tta tta atg gcg tcg agc gtc cgg tta aag ccg ctg aat tgt tgc cgt 1332
 Leu Leu Met Ala Ser Ser Val Arg Leu Lys Pro Leu Asn Cys Ser Arg
 50 55 60
 tta cct tgc gtg tac gcg cag gaa aca ctg acg ttc tta ctg acg cag 1380
 Leu Pro Cys Val Tyr Ala Gln Glu Thr Leu Thr Phe Leu Leu Thr Gln
 65 70 75
 aag aaa acg tgc gtc aaa aat tac gtg cag aag gag tgatgtaatg 1426
 Lys Lys Thr Cys Val Lys Asn Tyr Val Gln Lys Glu
 80 85 90
 tctaaaggta aaaaacgttc tggcgctcgc cctggctcgc cgcagccggtt gcgagggtact 1486
 aaaggcaagc gtaaaggcgc tcgtctttgg tatgtaggtg gtcaacaatt ttaattgcag 1546
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 35 40 45
 Gly Ala Leu Phe Asn Gly Ile Asn Ala Leu Asn Ala Tyr Asn Ala Ala
 50 55 60
 Leu Leu Thr Lys Ile Leu Lys Val Ser Val Glu Glu Phe Ser Pro Ser
 65 70 75 80
 Ile Ala Arg Glu Ile Tyr Glu Met Tyr Glu Ala Val Ser Met Gln Pro
 85 90 95
 Ser Leu Arg Ser Glu Tyr Glu Tyr Pro Val Phe Ser His Val Gln Ala
 100 105 110
 Gly Met Phe Ser Pro Lys Leu Arg Thr Phe Thr Lys Gly Asp Ala Glu
 115 120 125
 Arg Trp Val Ser Thr Thr Lys Lys Ala Ser Asp Ser Ala Phe Trp Leu
 130 135 140
 Glu Val Glu Gly Asn Ser Met Thr Ala Pro Thr Gly Ser Lys Pro Ser
 145 150 155 160
 Phe Pro Asp Gly Met Leu Ile Leu Val Asp Pro Glu Gln Ala Val Glu

165 170 175
 Pro Gly Asp Phe Cys Ile Ala Arg Leu Gly Gly Asp Glu Phe Thr Phe
 180 185 190
 Lys Lys Leu Ile Arg Asp Ser Gly Gln Val Phe Leu Gln Pro Leu Asn
 195 200 205
 Pro Gln Tyr Pro Met Ile Pro Cys Asn Glu Ser Cys Ser Val Val Gly
 210 215 220
 Lys Val Ile Ala Ser Gln Trp Pro Glu Glu Thr Phe Gly
 225 230 235

<210> 6
 <211> 91
 <212> PRT
 <213> pAW12 Fragment

<400> 6
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 20 25 30
 Lys Arg Pro Val Ser Ser Trp Lys Ala Leu Asn Leu Arg Lys Thr Leu
 35 40 45
 Leu Met Ala Ser Ser Val Arg Leu Lys Pro Leu Asn Cys Ser Arg Leu
 50 55 60
 Pro Cys Val Tyr Ala Gln Glu Thr Leu Thr Phe Leu Leu Thr Gln Lys
 65 70 75 80
 Lys Thr Cys Val Lys Asn Tyr Val Gln Lys Glu
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 <212> DNA
 <213> pCSJ Fragment

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aggccactga cttagcgataa ctttccccac aacggaacaa ctctcattgc atgggatcat 180
tgggtactgt ggggttagtg gttgtaaaaa cacctgaccg ctatccctga tcagtttctt 240
gaaggtaaac tcatcacccc caagtctggc tatgcagaaa tcacctggct caacagcctg 300
ctcagggtca acgagaatta acattccgtc aggaaagctt ggcttggagc ctgttggtgc 360
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gcttaccat ctctccgcat cacctttggt aaagggtcta agcttaggtg agaacaatccc 480
tgcctgaaca tgagaaaaaa cagggtactc atactcactt ctaagtgcg gctgcatact 540
aaccgcttca tacatctcgt agatttctct ggcgattgaa gggctaaatt cttcaacgct 600
aactttgaga atttttgtaa gcaatgcggc gttataagca tttaatgcat tgatgccatt 660
aaataaagca ccaacgcctg actgccccat ccccatcttg tctgcgacag attcctggga 720
taagccaagt tcatttttct ttttttcata aattgcttta aggcgacgtg cgtcctcaag 780
ctgctcttgt gttaatgggt tcttttttgt gctcatacgt taaatctatc accgcaaggg 840
ataaatatct aacaccgcgc gtgttgacta ttttacctct ggcggtgata atggttgcat 900
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gcaaaccaag acagctaaag atcctctaga gcgccggaa gagagtcaat tcagggtggt 1020
gaat gtg aaa cca gta acg tta tac gat gtc gca gag tat gcc ggt gtc 1069
Val Lys Pro Val Thr Leu Tyr Asp Val Ala Glu Tyr Ala Gly Val
1 5 10 15
tct tat cag acc gtt tcc cgc gtg gtg aac cag gcc agc cac gtt tct 1117
Ser Tyr Gln Thr Val Ser Arg Val Val Asn Gln Ala Ser His Val Ser
20 25 30
gcg aaa acg cgg gaa aaa gtg gaa gcg gcg atg gcg gag ctg aat tac 1165
Ala Lys Thr Arg Glu Lys Val Glu Ala Ala Met Ala Glu Leu Asn Tyr
35 40 45
att ccc aac cgc gtg gca caa caa ctg gcg ggc aaa cag tcg ttg ctg 1213
Ile Pro Asn Arg Val Ala Gln Gln Leu Ala Gly Lys Gln Ser Leu Leu
50 55 60
att ggc gtt gcc acc tcc agt ctg gcc ctg cac gcg ccg tcg caa att 1261
Ile Gly Val Ala Thr Ser Ser Leu Ala Leu His Ala Pro Ser Gln Ile
65 70 75
gtc gcg gcg att aaa tct cgc gcc gat caa ctg ggt gcc agc gtg gtg 1309
Val Ala Ala Ile Lys Ser Arg Ala Asp Gln Leu Gly Ala Ser Val Val
80 85 90 95
gtg tcg atg gta gaa cga agc ggc gtc gaa gcc tgt aaa gcg gcg gtg 1357
Val Ser Met Val Glu Arg Ser Gly Val Glu Ala Cys Lys Ala Ala Val
100 105 110

cac aat ctt ctc gcg caa cgc gtc agt ggg ctg atc att aac tat ccg	1405
His Asn Leu Leu Ala Gln Arg Val Ser Gly Leu Ile Ile Asn Tyr Pro	
115 120 125	
ctg gat gac cag gat gcc att gct gtg gaa gct gcc tgc act aat gtt	1453
Leu Asp Asp Gln Asp Ala Ile Ala Val Glu Ala Ala Cys Thr Asn Val	
130 135 140	
ccg gcg tta ttt ctt gat gtc tct gac cag aca ccc atc aac agt att	1501
Pro Ala Leu Phe Leu Asp Val Ser Asp Gln Thr Pro Ile Asn Ser Ile	
145 150 155	
att ttc tcc cat gaa gac ggt acg cga ctg ggc gtg gag cat ctg gtc	1549
Ile Phe Ser His Glu Asp Gly Thr Arg Leu Gly Val Glu His Leu Val	
160 165 170 175	
gca ttg ggt cac cag caa atc gcg ctg tta gcg ggc cca tta agt tct	1597
Ala Leu Gly His Gln Gln Ile Ala Leu Leu Ala Gly Pro Leu Ser Ser	
180 185 190	
gtc tcg gcg cgt ctg cgt ctg gct ggc tgg cat aaa tat ctc act cgc	1645
Val Ser Ala Arg Leu Arg Leu Ala Gly Trp His Lys Tyr Leu Thr Arg	
195 200 205	
aat caa att cag ccg ata gcg gaa cgg gaa ggc gac tgg agt gcc atg	1693
Asn Gln Ile Gln Pro Ile Ala Glu Arg Glu Gly Asp Trp Ser Ala Met	
210 215 220	
tcc ggt ttt caa caa acc atg caa atg ctg aat gag ggc atc gtt ccc	1741
Ser Gly Phe Gln Gln Thr Met Gln Met Leu Asn Glu Gly Ile Val Pro	
225 230 235	
act gcg atg ctg gtt gcc aac gat cag atg gcg ctg ggc gca atg cgc	1789
Thr Ala Met Leu Val Ala Asn Asp Gln Met Ala Leu Gly Ala Met Arg	
240 245 250 255	
gcc att acc gag tcc ggg ctg cgc gtt ggt gcg gat atc tcg gta gtg	1837
Ala Ile Thr Glu Ser Gly Leu Arg Val Gly Ala Asp Ile Ser Val Val	
260 265 270	
gga tac gac gat acc gaa gac agc tca tgt tat atc ccg ccg tca acc	1885
Gly Tyr Asp Asp Thr Glu Asp Ser Ser Cys Tyr Ile Pro Pro Ser Thr	
275 280 285	
acc atc aaa cag gat ttt cgc ctg ctg ggg caa acc agc gtg gac cgc	1933
Thr Ile Lys Gln Asp Phe Arg Leu Leu Gly Gln Thr Ser Val Asp Arg	
290 295 300	
ttg ctg caa ctc tct cag ggc cag gcg gtg aag ggc aat cag ctg ttg	1981
Leu Leu Gln Leu Ser Gln Gly Gln Ala Val Lys Gly Asn Gln Leu Leu	
305 310 315	
ccc gtc tca ctg gtg aaa aga aaa acc acc ctg gcg ccc aat acg caa	2029
Pro Val Ser Leu Val Lys Arg Lys Thr Thr Leu Ala Pro Asn Thr Gln	
320 325 330 335	
acc gcc tct ccc cgc gcg ttg gcc gat tca tta atg cag ctg gca cga	2077
Thr Ala Ser Pro Arg Ala Leu Ala Asp Ser Leu Met Gln Leu Ala Arg	
340 345 350	

a!
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cag gtt tcc cga ctg gaa agc ggg cag tgagcgcaac gcaattaatg 2124
 Gln Val Ser Arg Leu Glu Ser Gly Gln
 355 360

tgagtttagct cactcattag gcaccccgagg ctttacactt tatgcttccg gctcgtatgt 2184
 tgtgtggaat tgtgagcgga taacaatttc acacaggaaa cagctctgca ggcattgcaag 2244
 cttatcgaat tctcattcag gcttctgccc ttttggaattt aaccgaagat gatttcgatt 2304
 ttctgacgag taacaaagtt tggattgcta ctgaccgctc tegtgtctgt cgctgcgttg 2364
 aggcttgcgt tt atg gta cgc tgg act ttg tgg gat acc ctc gct ttc ctg 2415
 Met Val Arg Trp Thr Leu Trp Asp Thr Leu Ala Phe Leu
 365 370

ctc ctg ttg agt tta ttg ctg ccg tca ttg ctt att atg ttc atc ccg 2463
 Leu Leu Leu Ser Leu Leu Pro Ser Leu Leu Ile Met Phe Ile Pro
 375 380 385

tca aca ttc aaa cgg cct gtc tca tca tgg aag gcg ctg aat tta cgg 2511
 Ser Thr Phe Lys Arg Pro Val Ser Ser Trp Lys Ala Leu Asn Leu Arg
 390 395 400 405

aaa aca tta tta atg gcg tgc agc gtc cgg tta aag ccg ctg aat tgt 2559
 Lys Thr Leu Leu Met Ala Ser Ser Val Arg Leu Lys Pro Leu Asn Cys
 410 415 420

tcg cgt tta cct tgc gtg tac gcg cag gaa aca ctg acg ttc tta ctg 2607
 Ser Arg Leu Pro Cys Val Tyr Ala Gln Glu Thr Leu Thr Phe Leu Leu
 425 430 435

acg cag aag aaa acg tgc gtc aaa aat tac gtg cag aag gag 2649
 Thr Gln Lys Lys Thr Cys Val Lys Asn Tyr Val Gln Lys Glu
 440 445 450

tgatgtaatg tctaaaggta aaaaacgttc tggcgctcgc cctgggtcgtc cgcagccggtt 2709

gcgaggtact aaaggcaagc gtaaaggcgc tcgtctttgg tatgtagggtg gtcaacaatt 2769

ttaattgcag gggcttcggc ccttacttga ggataaatta tgtctaatat tcaaactggc 2829

gccga 2834

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 <213> pCSJ Fragment

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 Arg Arg Leu Lys Ala Ile Tyr Glu Lys Lys Lys Asn Glu Leu Gly Leu
 20 25 30
 Ser Gln Glu Ser Val Ala Asp Lys Met Gly Met Gly Gln Ser Gly Val
 35 40 45

a!
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Gly Ala Leu Phe Asn Gly Ile Asn Ala Leu Asn Ala Tyr Asn Ala Ala
 50 55 60
 Leu Leu Thr Lys Ile Leu Lys Val Ser Val Glu Glu Phe Ser Pro Ser
 65 70 75 80
 Ile Ala Arg Glu Ile Tyr Glu Met Tyr Glu Ala Val Ser Met Gln Pro
 85 90 95
 Ser Leu Arg Ser Glu Tyr Glu Tyr Pro Val Phe Ser His Val Gln Ala
 100 105 110
 Gly Met Phe Ser Pro Lys Leu Arg Thr Phe Thr Lys Gly Asp Ala Glu
 115 120 125
 Arg Trp Val Ser Thr Thr Lys Lys Ala Ser Asp Ser Ala Phe Trp Leu
 130 135 140
 Glu Val Glu Gly Asn Ser Met Thr Ala Pro Thr Gly Ser Lys Pro Ser
 145 150 155 160
 Phe Pro Asp Gly Met Leu Ile Leu Val Asp Pro Glu Gln Ala Val Glu
 165 170 175
 Pro Gly Asp Phe Cys Ile Ala Arg Leu Gly Gly Asp Glu Phe Thr Phe
 180 185 190
 Lys Lys Leu Ile Arg Asp Ser Gly Gln Val Phe Leu Gln Pro Leu Asn
 195 200 205
 Pro Gln Tyr Pro Met Ile Pro Cys Asn Glu Ser Cys Ser Val Val Gly
 210 215 220
 Lys Val Ile Ala Ser Gln Trp Pro Glu Glu Thr Phe Gly
 225 230 235

<210> 9
 <211> 360
 <212> PRT
 <213> pCSJ Fragment

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 Lys Thr Arg Glu Lys Val Glu Ala Ala Met Ala Glu Leu Asn Tyr Ile
 35 40 45
 Pro Asn Arg Val Ala Gln Gln Leu Ala Gly Lys Gln Ser Leu Leu Ile
 50 55 60
 Gly Val Ala Thr Ser Ser Leu Ala Leu His Ala Pro Ser Gln Ile Val
 65 70 75 80
 Ala Ala Ile Lys Ser Arg Ala Asp Gln Leu Gly Ala Ser Val Val Val

85

90

95

Ser Met Val Glu Arg Ser Gly Val Glu Ala Cys Lys Ala Ala Val His
 100 105 110
 Asn Leu Leu Ala Gln Arg Val Ser Gly Leu Ile Ile Asn Tyr Pro Leu
 115 120 125
 Asp Asp Gln Asp Ala Ile Ala Val Glu Ala Ala Cys Thr Asn Val Pro
 130 135 140
 Ala Leu Phe Leu Asp Val Ser Asp Gln Thr Pro Ile Asn Ser Ile Ile
 145 150 155 160
 Phe Ser His Glu Asp Gly Thr Arg Leu Gly Val Glu His Leu Val Ala
 165 170 175
 Leu Gly His Gln Gln Ile Ala Leu Leu Ala Gly Pro Leu Ser Ser Val
 180 185 190
 Ser Ala Arg Leu Arg Leu Ala Gly Trp His Lys Tyr Leu Thr Arg Asn
 195 200 205
 Gln Ile Gln Pro Ile Ala Glu Arg Glu Gly Asp Trp Ser Ala Met Ser
 210 215 220
 Gly Phe Gln Gln Thr Met Gln Met Leu Asn Glu Gly Ile Val Pro Thr
 225 230 235 240
 Ala Met Leu Val Ala Asn Asp Gln Met Ala Leu Gly Ala Met Arg Ala
 245 250 255
 Ile Thr Glu Ser Gly Leu Arg Val Gly Ala Asp Ile Ser Val Val Gly
 260 265 270
 Tyr Asp Asp Thr Glu Asp Ser Ser Cys Tyr Ile Pro Pro Ser Thr Thr
 275 280 285
 Ile Lys Gln Asp Phe Arg Leu Leu Gly Gln Thr Ser Val Asp Arg Leu
 290 295 300
 Leu Gln Leu Ser Gln Gly Gln Ala Val Lys Gly Asn Gln Leu Leu Pro
 305 310 315 320
 Val Ser Leu Val Lys Arg Lys Thr Thr Leu Ala Pro Asn Thr Gln Thr
 325 330 335
 Ala Ser Pro Arg Ala Leu Ala Asp Ser Leu Met Gln Leu Ala Arg Gln
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 Val Ser Arg Leu Glu Ser Gly Gln
 355 360

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<211> 91

<212> PRT

<213> pCSJ Fragment

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Met Val Arg Trp Thr Leu Trp Asp Thr Leu Ala Phe Leu Leu Leu Leu
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20 25 30

Lys Arg Pro Val Ser Ser Trp Lys Ala Leu Asn Leu Arg Lys Thr Leu
35 40 45

Leu Met Ala Ser Ser Val Arg Leu Lys Pro Leu Asn Cys Ser Arg Leu
50 55 60

Pro Cys Val Tyr Ala Gln Glu Thr Leu Thr Phe Leu Leu Thr Gln Lys
65 70 75 80

Lys Thr Cys Val Lys Asn Tyr Val Gln Lys Glu
85 90

<210> 11

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
primer

<400> 11

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37

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